

**AMENDMENTS TO THE CLAIMS**

The following Listing of the Claims replaces all prior claims in the application.

1. (Withdrawn) A method for detecting a mutation in presenilin associated membrane protein (PAMP) associated with a neuropsychiatric or neurodevelopmental disorder, which method comprises detecting a variation in a sequence of a gene encoding PAMP obtained from an individual diagnosed with or suspected of having said disorder.
2. (Withdrawn) The method of claim 1, wherein the disorder is schizophrenia.
3. (Withdrawn) A method for diagnosing individuals predisposed to or having a neuropsychiatric or neurodevelopmental disorder, which method comprises detecting a mutation in a gene encoding PAMP obtained from an individual.
4. (Withdrawn) The method of claim 3, wherein the disorder is schizophrenia.
5. (Withdrawn) The method according to claim 3, wherein detection of the mutation comprises measuring a level of transcriptional activity of the gene.
6. (Withdrawn) The method according to claim 3, wherein detection of the mutation comprises measuring PAMP activity.
7. (Withdrawn) The method of claim 6, wherein said PAMP activity comprises PAMP expression level or activity of a product of a PAMP modified substrate.





18. (Previously Presented) The method of claim 10, wherein the PAMP substrate is presenilin 1.
19. (Previously Presented) The method of claim 10, wherein the PAMP substrate is  $\beta$ APP.
20. (Previously Presented) The method of claim 10, wherein the PAMP amino acid sequence comprises at least one amino acid sequence motif starting at a position corresponding to a residue of SEQ ID NO:14 selected from the group consisting of NKTA at residue 45, NATH at residue 55, NETK at residue 187, NGSA at residue 204, NQSQ at residue 417, NISG at residue 435, NNSW at residue 530, NTTY at residue 562, NLTG at residue 573, NLTR at residue 580, SGAG at residue 404, GCQSSI at residue 61, GNGLAY at residue 167, GAESAV at residue 294, GVV LAD at residue 438, TSR at residue 115, SSR at residue 340, SQK at residue 384, TRLD at residue 280, SFVE at residue 361, SIYD at residue 455, SSTE at residue 641, and combinations thereof.
21. (Previously Presented) The method of claim 20, wherein the PAMP amino acid sequence comprises the amino acid sequence motifs, starting at positions corresponding to residues of SEQ ID NO:14, NKTA at residue 45, NATH at residue 55, NETK at residue 187, NGSA at residue 204, NQSQ at residue 417, NISG at residue 435, NNSW at residue 530, NTTY at residue 562, NLTG at residue 573, NLTR at residue 580, SGAG at residue 404, GCQSSI at residue 61, GNGLAY at residue 167, GAESAV at residue 294, GVV LAD at residue 438, TSR at residue 115, SSR at residue 340, SQK at residue 384, TRLD at residue 280, SFVE at residue 361, SIYD at residue 455, and SSTE at residue 641.

22. (Previously Presented) The method of claim 21, wherein the PAMP has the amino acid sequence of SEQ ID NO:16.
23. (Previously Presented) The method of claim 21, wherein the PAMP has the amino acid sequence of SEQ ID NO:14.